

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/052,798B
Source: ifw16
Date Processed by STIC: 1/5/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/05/2005

PATENT APPLICATION: US/10/052,798B

TIME: 16:24:14

Input Set : A:\P1101R2D1.txt

Output Set: N:\CRF4\01052005\J052798B.raw

SEQUENCE LISTING

9 (1) GENERAL INFORMATION:

11 (i) APPLICANT: Adams, Camilia W.
 12 Ashkenazi, Avi J.
 13 Chuntharapai, Anan
 14 Kim, Kyung J.

16 (ii) TITLE OF INVENTION: Inducing Apoptosis Using Anti-Apo-2 Antibodies

18 (iii) NUMBER OF SEQUENCES: 19

20 (iv) CORRESPONDENCE ADDRESS:
 21 (A) ADDRESSEE: Genentech, Inc.
 22 (B) STREET: 1 DNA Way
 23 (C) CITY: South San Francisco
 24 (D) STATE: California
 25 (E) COUNTRY: USA
 26 (F) ZIP: 94080

28 (v) COMPUTER READABLE FORM:
 29 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 30 (B) COMPUTER: IBM PC compatible
 31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 32 (D) SOFTWARE: WinPatin (Genentech)

34 (vi) CURRENT APPLICATION DATA:
 C--> 35 (A) APPLICATION NUMBER: US/10/052,798B
 C--> 36 (B) FILING DATE: 02-Nov-2001
 37 (C) CLASSIFICATION:

47 (vii) PRIOR APPLICATION DATA:
 40 (A) APPLICATION NUMBER: 09/079029
 41 (B) FILING DATE: 14-MAY-1998
 44 (A) APPLICATION NUMBER: 60/046615
 45 (B) FILING DATE: 15-MAY-1997
 48 (A) APPLICATION NUMBER: 60/074119
 49 (B) FILING DATE: 09-FEB-1998

51 (viii) ATTORNEY/AGENT INFORMATION:
 52 (A) NAME: Marschang, Diane L.
 53 (B) REGISTRATION NUMBER: 35,600
 54 (C) REFERENCE/DOCKET NUMBER: P1101R2D1

56 (ix) TELECOMMUNICATION INFORMATION:
 57 (A) TELEPHONE: 650/225-5416
 58 (B) TELEFAX: 650/952-9881

59 (2) INFORMATION FOR SEQ ID NO: 1:
 61 (i) SEQUENCE CHARACTERISTICS:
 62 (A) LENGTH: 411 amino acids
 63 (B) TYPE: Amino Acid
 64 (D) TOPOLOGY: Linear

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66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68  Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
69      1          5          10          15
71  Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
72          20          25          30
74  Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
75          35          40          45
77  Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
78          50          55          60
80  Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
81          65          70          75
83  Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
84          80          85          90
86  Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
87          95          100          105
89  His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
90          110          115          120
92  Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
93          125          130          135
95  Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
96          140          145          150
98  Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
99          155          160          165
101  Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
102          170          175          180
104  Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
105          185          190          195
107  Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
108          200          205          210
110  Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp
111          215          220          225
113  Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
114          230          235          240
116  Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
117          245          250          255
119  Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
120          260          265          270
122  Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
123          275          280          285
125  Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
126          290          295          300
128  Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
129          305          310          315
131  Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
132          320          325          330
134  Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
135          335          340          345
137  Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
138          350          355          360

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140 Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
 141 365 370 375
 143 Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
 144 380 385 390
 146 Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 147 395 400 405
W--> 149 Ala Asp Ser Ala Xaa Ser
 150 410
 152 (2) INFORMATION FOR SEQ ID NO: 2:
 154 (i) SEQUENCE CHARACTERISTICS:
 155 (A) LENGTH: 1799 base pairs
 156 (B) TYPE: Nucleic Acid
 157 (C) STRANDEDNESS: Single
 158 (D) TOPOLOGY: Linear
 160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 163 CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50
 165 GCGCCCAAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100
 167 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
 168 Met Glu
 169 1
 171 CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
 172 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
 173 5 10 15
 175 AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
 176 Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
 177 20 25
 179 AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
 180 Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
 181 30 35 40
 183 GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
 184 Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
 185 45 50
 187 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
 188 Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
 189 55 60 65
 191 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
 192 Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 193 70 75 80
 195 TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
 196 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
 197 85 90
 199 TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
 200 Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
 201 95 100 105
 203 TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
 204 Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
 205 110 115
 207 GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
 208 Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr

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209 120 125 130
211 AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
212 Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
213 135 140 145
215 GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
216 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
217 150 155
219 GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
220 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
221 160 165 170
223 CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
224 Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
225 175 180
227 ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
228 Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
229 185 190 195
231 GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
232 Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
233 200 205 210
235 GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
236 Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
237 215 220
239 GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
240 Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
241 225 230 235
243 GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
244 Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
245 240 245
247 TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
248 Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
249 250 255 260
251 CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
252 Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
253 265 270 275
255 CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
256 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
257 280 285
259 GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
260 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
261 290 295 300
263 GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
264 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
265 305 310
267 GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
268 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
269 315 320 325
271 CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
272 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
273 330 335 340

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275 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
276 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
277           345           350
279 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
280 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
281       355           360           365
283 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
284 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
285           370           375
287 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
288 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
289       380           385           390
291 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
292 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
293       395           400           405
295 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
W--> 296 Ala Asp Ser Ala Xaa Ser
297           410 411
299 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
301 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500
303 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACCTT TTCCTGCAC 1550
305 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600
307 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTGTT TGGGATGTCA 1650
309 TTGTTTTTAC AGCACTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700
311 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAG 1750
313 GCGGCGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799
315 (2) INFORMATION FOR SEQ ID NO: 3:
317     (i) SEQUENCE CHARACTERISTICS:
318         (A) LENGTH: 70 base pairs
319         (B) TYPE: Nucleic Acid
320         (C) STRANDEDNESS: Single
321         (D) TOPOLOGY: Linear
323     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
326 GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50
328 GCTAAAGCTG AGGCAGCGGG 70
330 (2) INFORMATION FOR SEQ ID NO: 4:
332     (i) SEQUENCE CHARACTERISTICS:
333         (A) LENGTH: 29 base pairs
334         (B) TYPE: Nucleic Acid
335         (C) STRANDEDNESS: Single
336         (D) TOPOLOGY: Linear
338     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
341 ATCAGGGACT TTCCGCTGGG GACTTTCCG 29
343 (2) INFORMATION FOR SEQ ID NO: 5:
345     (i) SEQUENCE CHARACTERISTICS:
346         (A) LENGTH: 30 base pairs
347         (B) TYPE: Nucleic Acid
348         (C) STRANDEDNESS: Single
349         (D) TOPOLOGY: Linear

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